

ySIR2	1	THKVI	1	THKVI	30	THKVI
yHS1	1	THKVI	1	THKVI	31	THKVI
mSIR2α	33	THKVI	33	THKVI	33	THKVI
Cobb	7	THKVI	7	THKVI	7	THKVI
		***		***		***
ySIR2	31	LVLEGA	31	LVLEGA	61	LVLEGA
yHS1	31	LVLEGA	31	LVLEGA	61	LVLEGA
mSIR2α	34	LVLEGA	34	LVLEGA	66	LVLEGA
Cobb	8	LVLEGA	8	LVLEGA	38	LVLEGA
		***		***		***
ySIR2	62	PDPCD	62	PDPCD	93	PDPCD
yHS1	62	PDPCD	62	PDPCD	93	PDPCD
mSIR2α	67	PDPCD	67	PDPCD	98	PDPCD
Cobb	39	PDPCD	39	PDPCD	68	PDPCD
		***		***		***
ySIR2	94	YSRPL	94	YSRPL	125	YSRPL
yHS1	94	YSRPL	94	YSRPL	125	YSRPL
mSIR2α	99	YSRPL	99	YSRPL	130	YSRPL
Cobb	69	YSRPL	69	YSRPL	101	YSRPL
		***		***		***
ySIR2	126	AGSTID	126	AGSTID	158	AGSTID
yHS1	126	AGSTID	126	AGSTID	158	AGSTID
mSIR2α	131	AGSTID	131	AGSTID	161	AGSTID
Cobb	102	AGSTID	102	AGSTID	132	AGSTID
		***		***		***
ySIR2	139	NKTHN	139	NKTHN	191	NKTHN
yHS1	139	NKTHN	139	NKTHN	191	NKTHN
mSIR2α	162	NKTHN	162	NKTHN	176	NKTHN
Cobb	133	NKTHN	133	NKTHN	156	NKTHN
		***		***		***
ySIR2	192	ASQGS	192	ASQGS	224	ASQGS
yHS1	192	ASQGS	192	ASQGS	224	ASQGS
mSIR2α	177	ASQGS	177	ASQGS	219	ASQGS
Cobb	189	ASQGS	189	ASQGS	186	ASQGS
		***		***		***
ySIR2	225	KSTPL	225	KSTPL	250	KSTPL
yHS1	225	KSTPL	225	KSTPL	247	KSTPL
mSIR2α	198	KSTPL	198	KSTPL	222	KSTPL
Cobb	187	KSTPL	187	KSTPL	215	KSTPL
		***		***		***
ySIR2	263	SEITM	263	SEITM	277	SEITM
yHS1	263	SEITM	263	SEITM	267	SEITM
mSIR2α	238	SEITM	238	SEITM	240	SEITM
Cobb	230	SEITM	230	SEITM	233	SEITM

Figure 2C

core domain

Figure 2D

1	MADEVALA	LQAA	GPSA	AA	AMEA	ASQPADEPLRKR	PRRDC
41	PGLRSP	GESA	VA	PA	AAGCEA	ASAA	PAALWREA
81	ASARE	APAT	AVAGD	GN	SG	GLRRE	PRAADD
121	DEAAAA	AAAA	AI	GYRDN	LL	TDGL	TNGFHS
161	SHASS	DWTP	PR	PI	GPYT	FVQ	QHLMIG
201	TIPPE	LDDMT	LQ	IV	IN	LSEPP	KRKRKD
241	LLOECK	IV	LTGAG	VS	VC	GIPDF	RSR
281	DLDPQ	AMFD	IEY	RK	DP	PF	FKFAKE
321	FIALSD	KEGK	LL	RNYT	QN	IDT	LEQV
361	ASCLICK	YKV	DCEA	VR	GD	IFN	QVVP
401	PEI	VFFGEN	LPEQ	HR	AM	KYDK	DEVD
441	ALIPSS	I	HEV	PQ	I	LNREP	LPHL
481	LCHRL	GG	EYAK	L	CNP	VK	LSEITEK
521	PTPLH	I	SE	SS	PER	VP	QDS
561	VSESS	CEEK	PQ	EV	Q	T	SRN
601	NERTSV	AE	TVR	K	WPN	R	LAKE
641	IFHGA	E	VY	SD	SE	DD	VLS
681	DESE	I	EE	F	Y	N	G
721	IATRQ	E	L	T	D	V	N

Figure 2A

Western

IVT

IP

no RNA

IVTmSIR2α

rabbit IgG

c-mycSIR2α

arrowhead

asterisk

Figure 2B

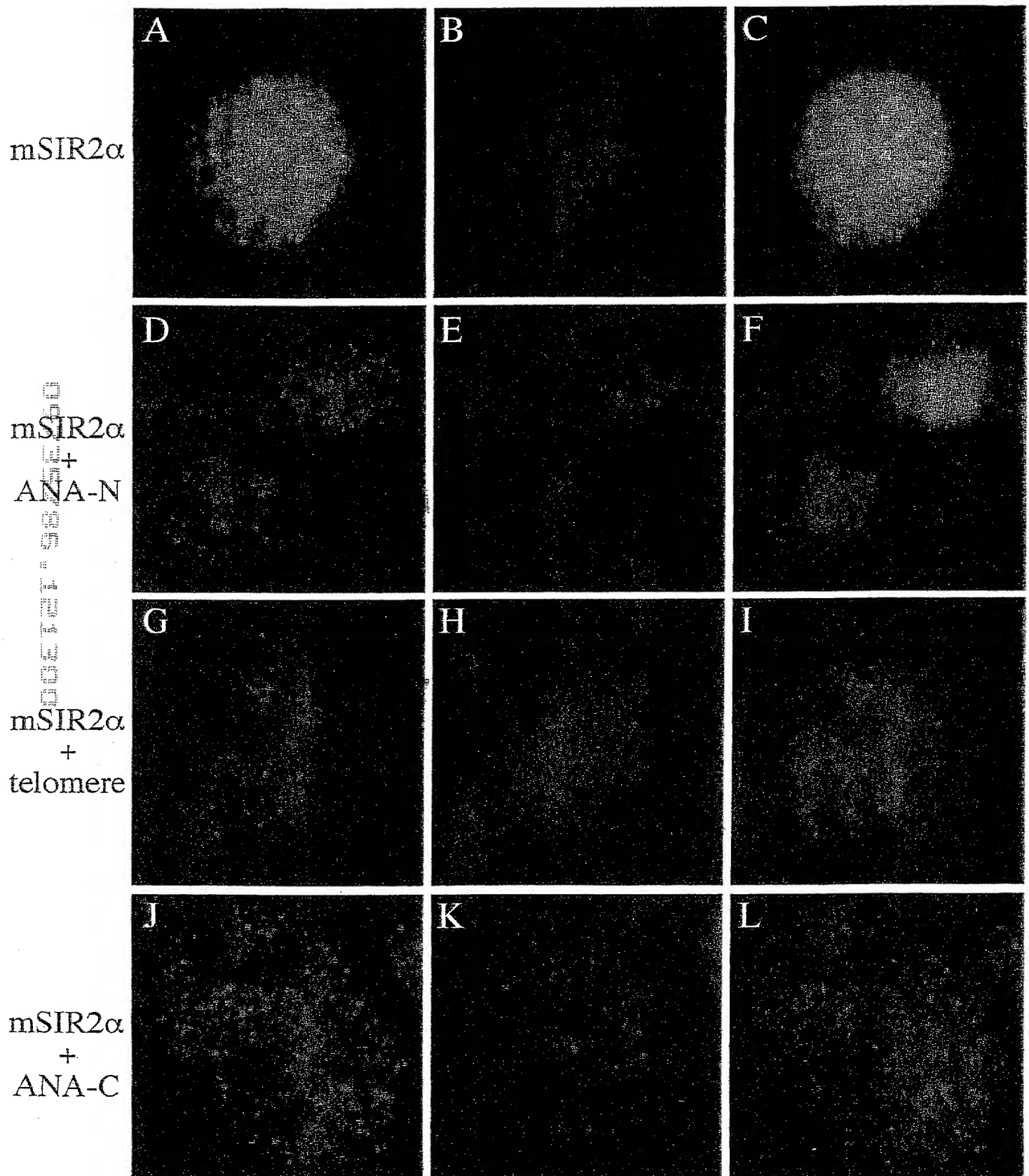


Figure 3

006127 5925E60

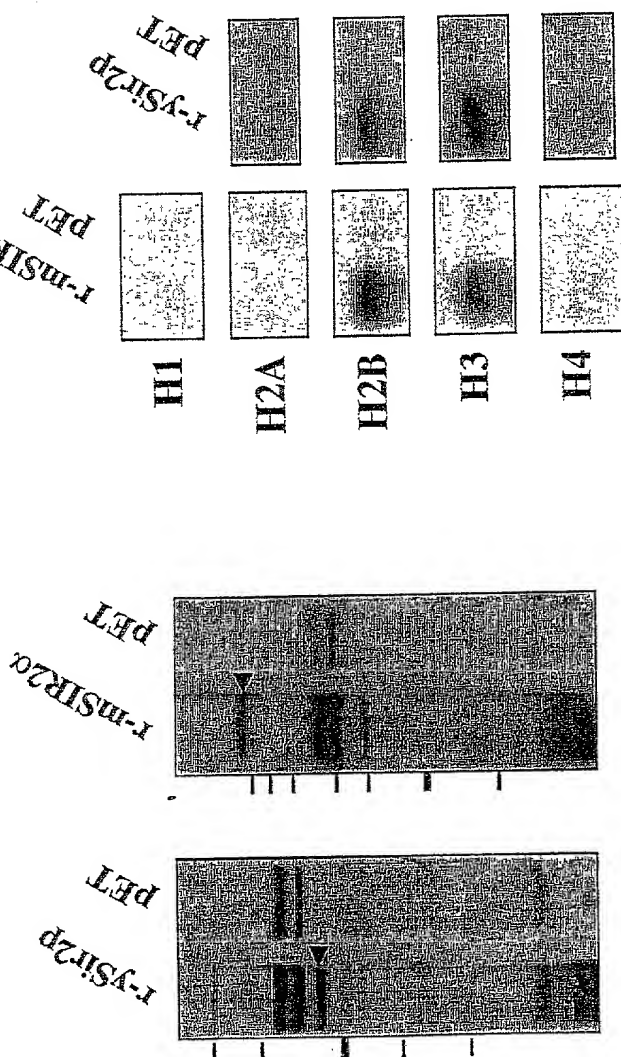


Figure 4A

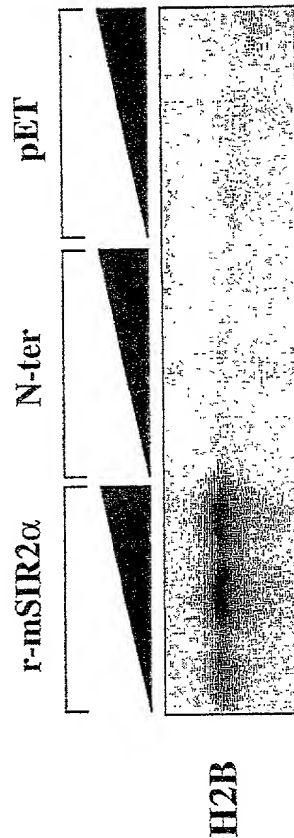


Figure 4B

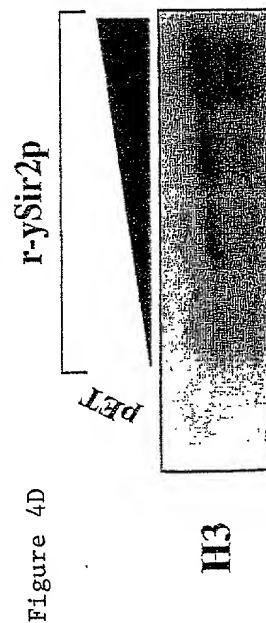


Figure 4D

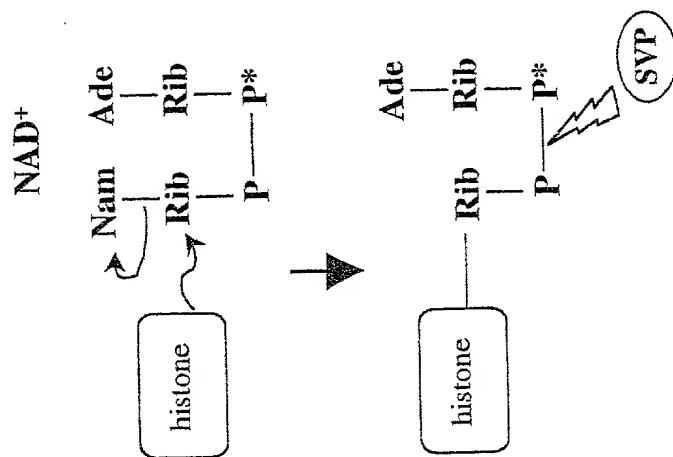


Figure 4C

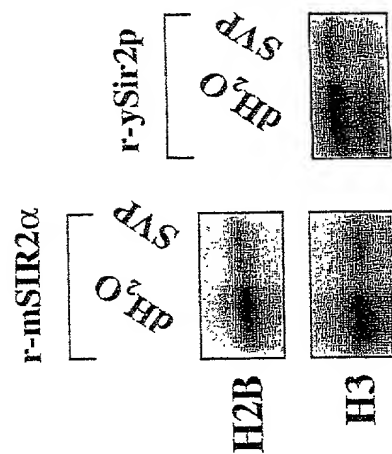


Figure 4E

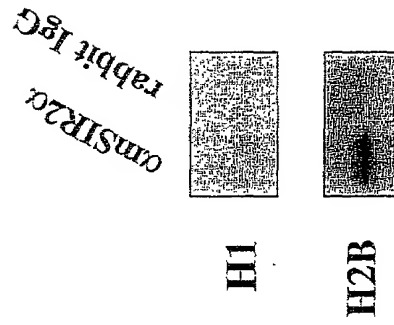


Figure 4G

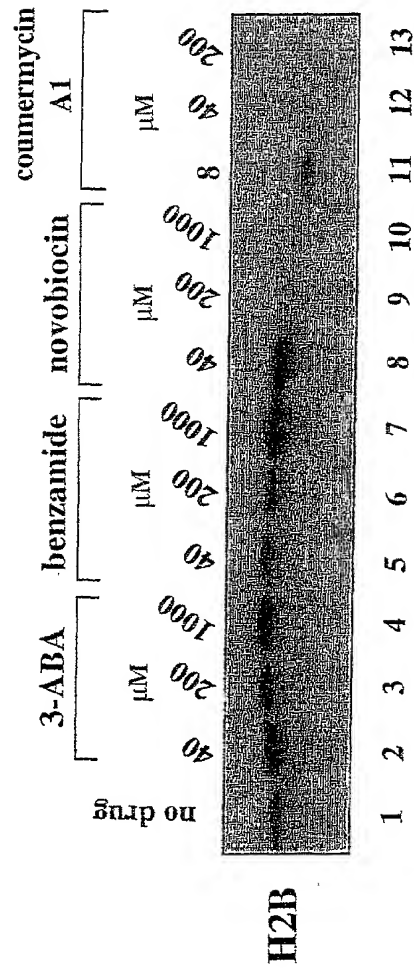


Figure 4F

0050.1618-001

H3	unAc	*	*	*
	diAc	ARTKQTARKSTGGKAPRKQLC		
H4		*	*	*
	monoAc	SGRGKGGKGLGKGGAKRHRC	5 8 12 16	*
		*	*	*
	tetraAc	AGGKGGKGMGKVGAKRHSC		*

Figure 5A

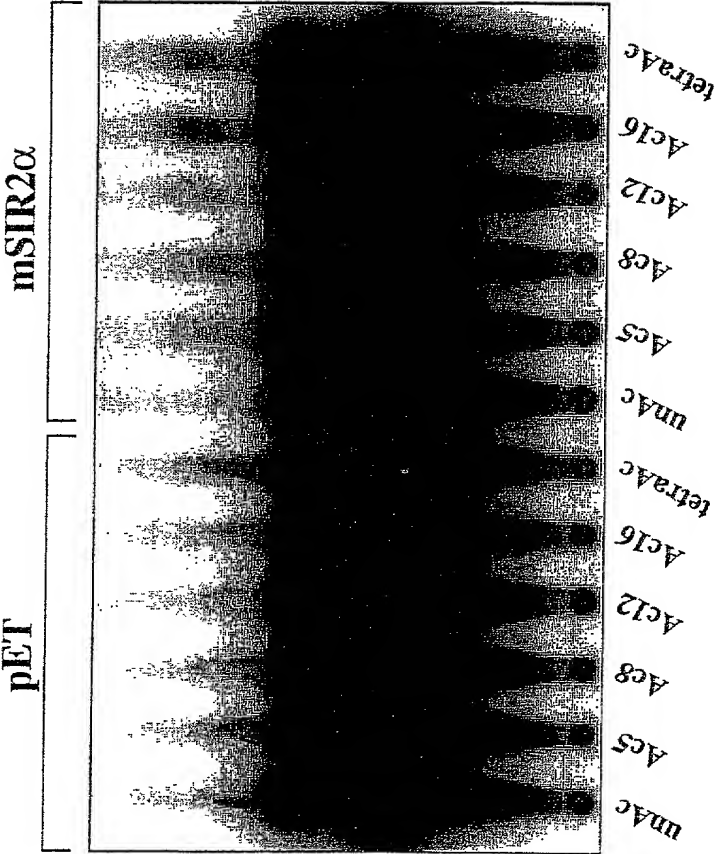


Figure 5C

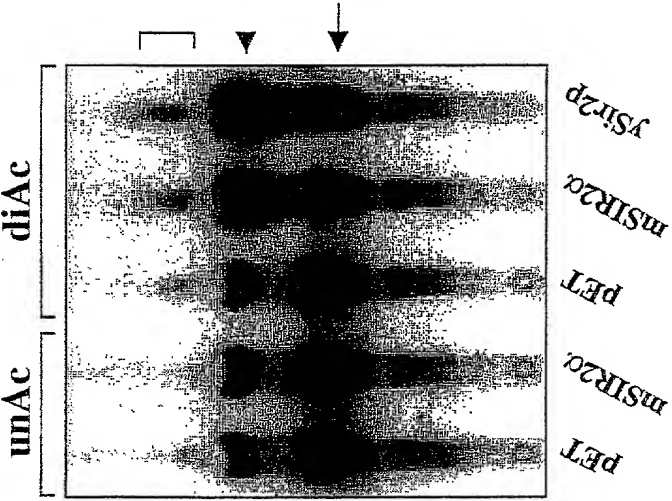
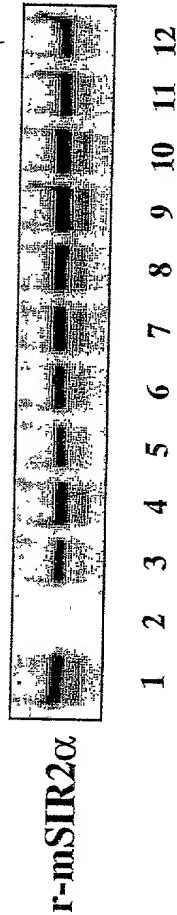
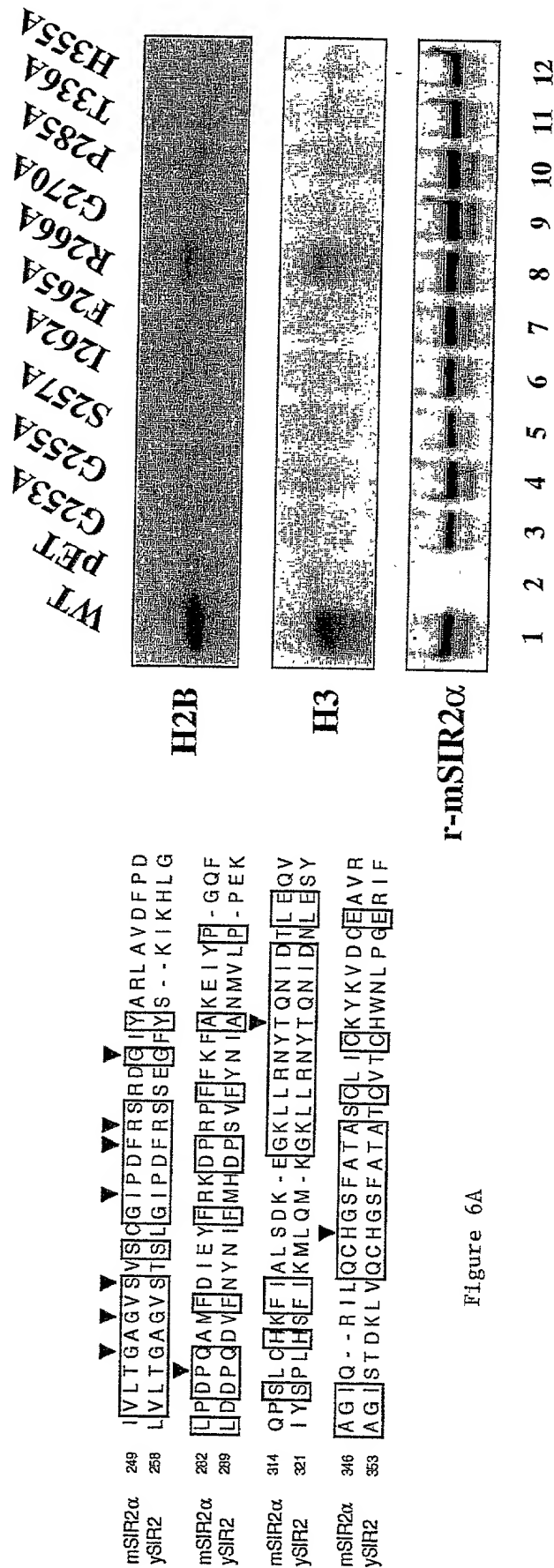
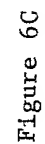
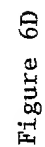


Figure 5B





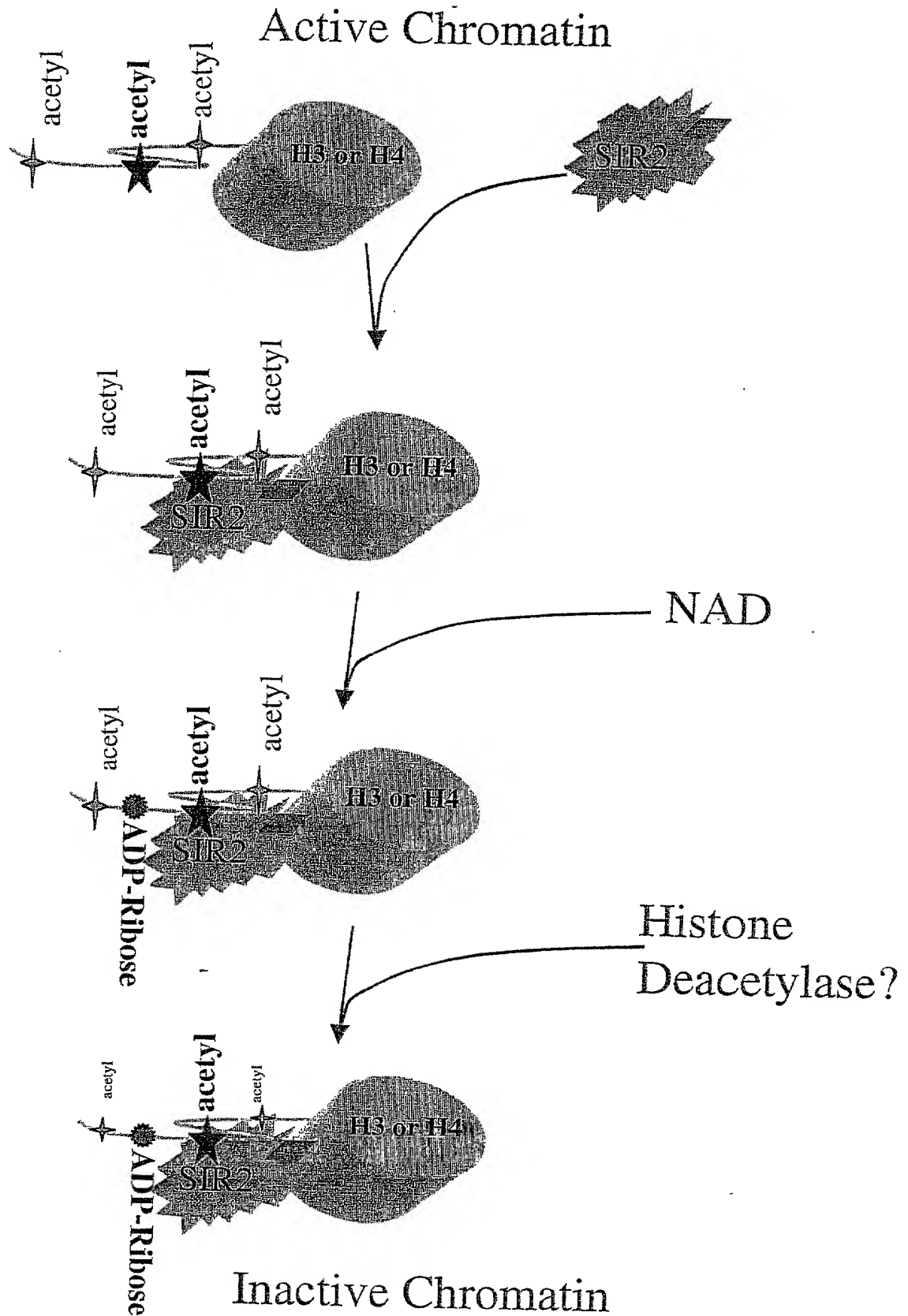


Figure 7

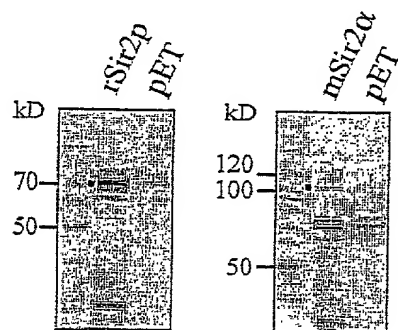


Figure 8a

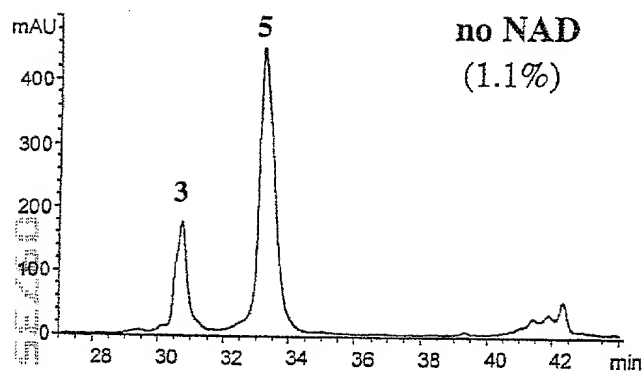


Figure 8b

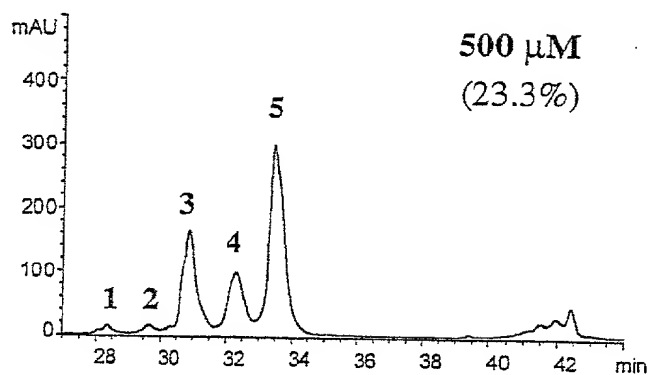


Figure 8e

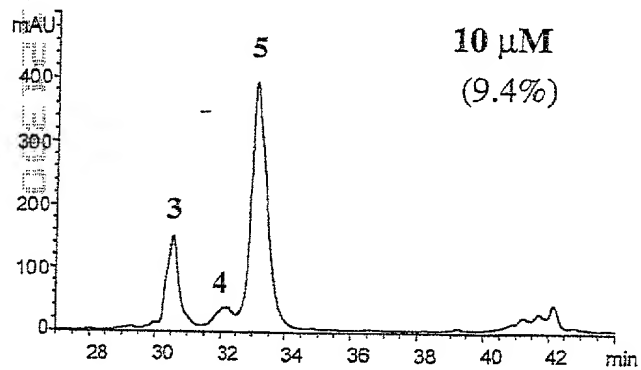


Figure 8c

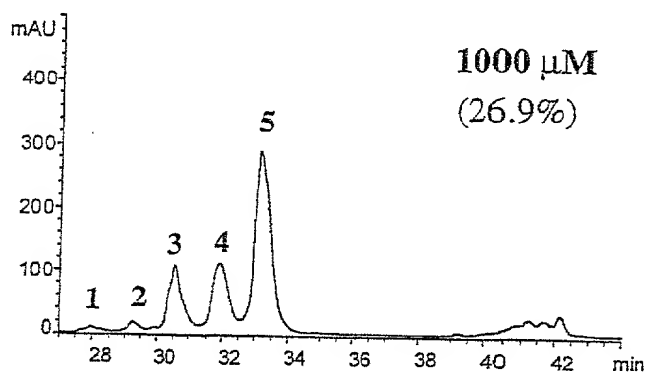


Figure 8f

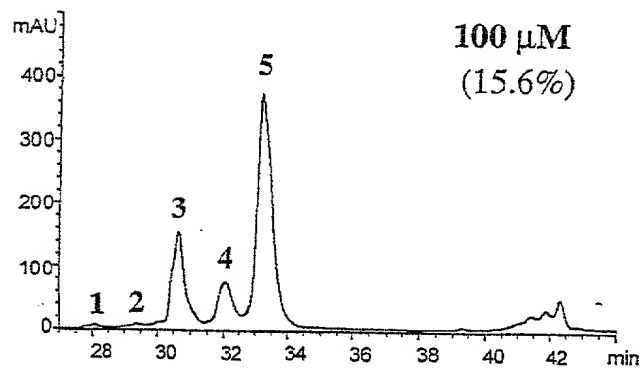


Figure 8d

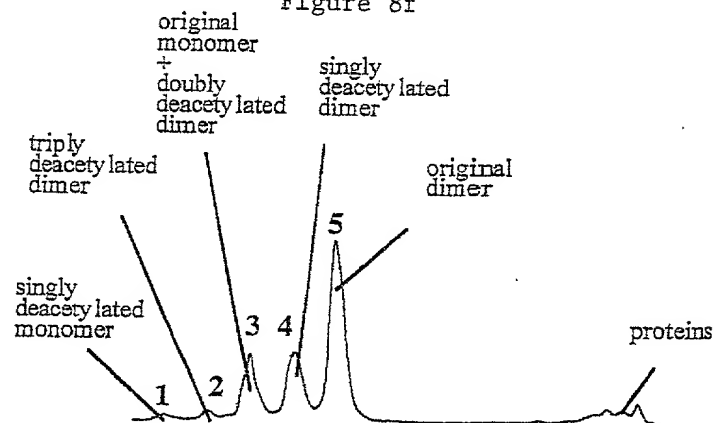


Figure 8g

Figure 9a

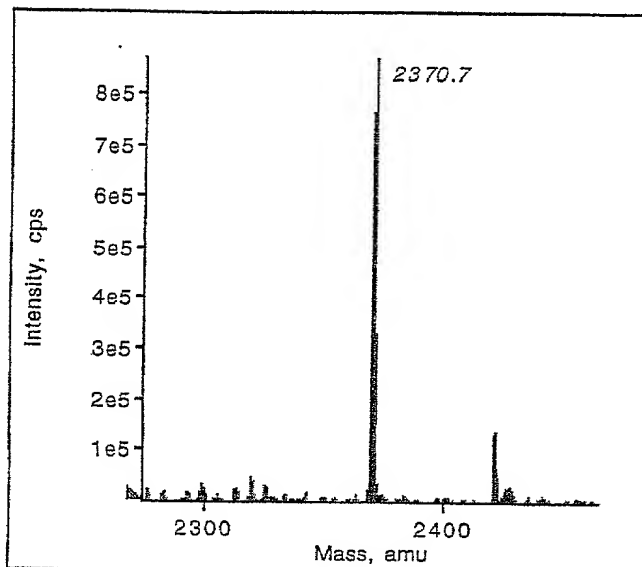


Figure 9b

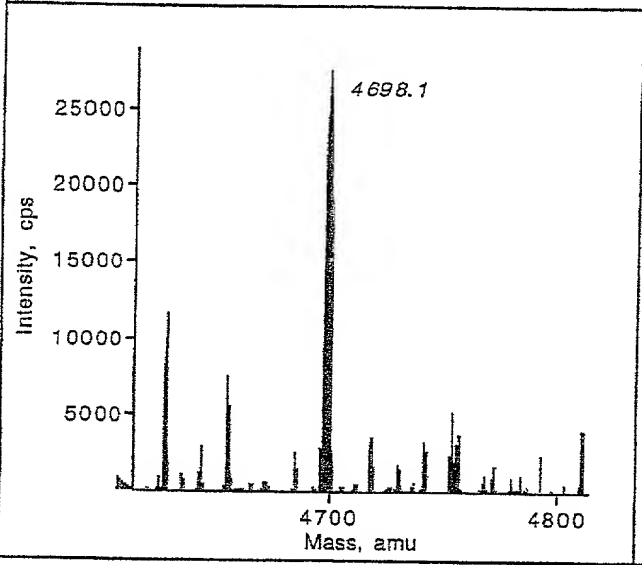
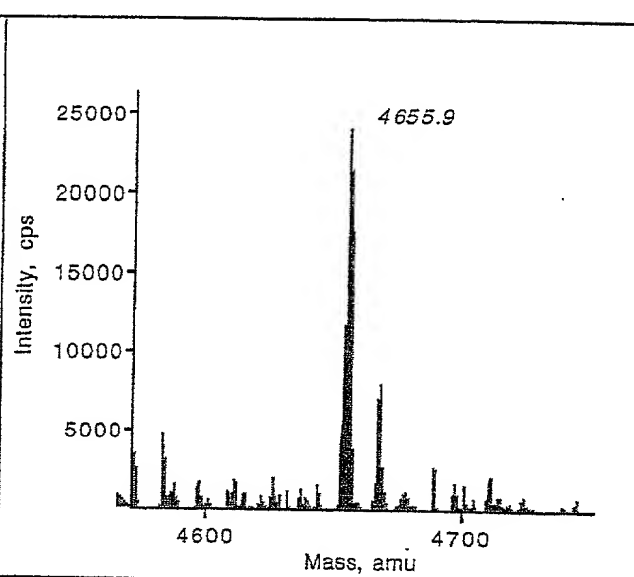


Figure 9c

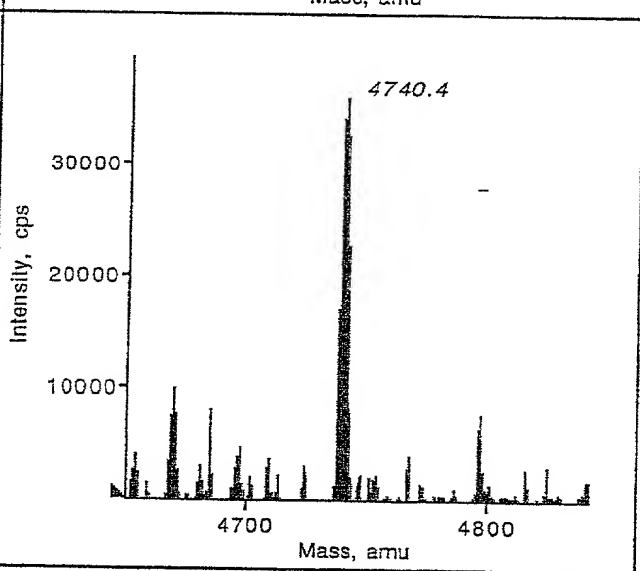


Figure 9d

0050.1618-001

peak 4

peak 5

9

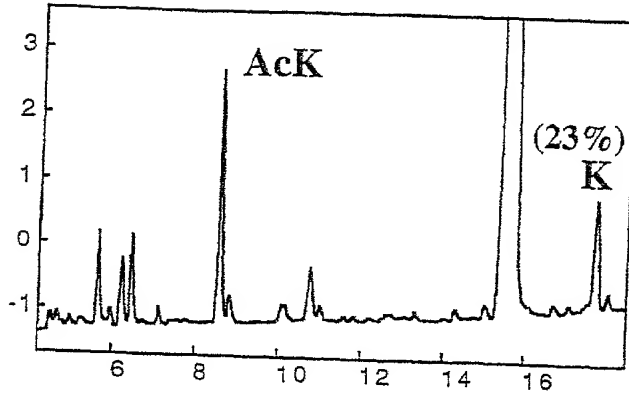


Figure 10a

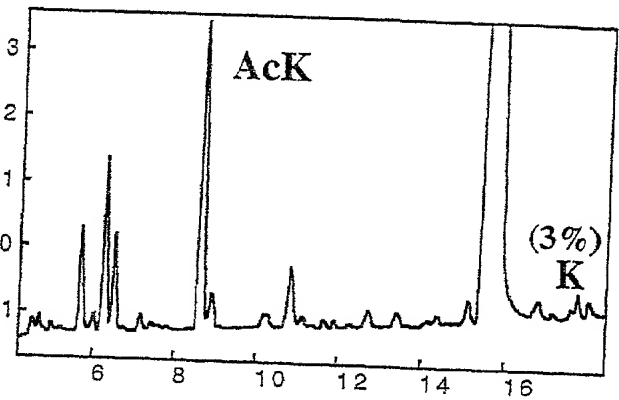


Figure 10d

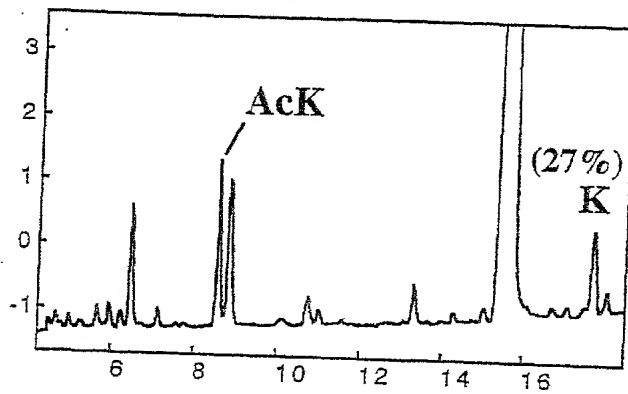


Figure 10b

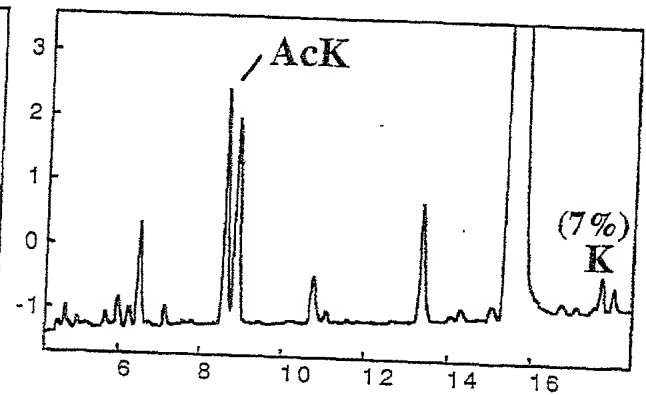


Figure 10e

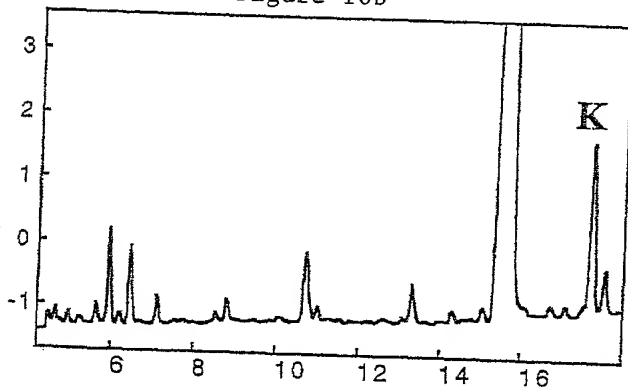


Figure 10c

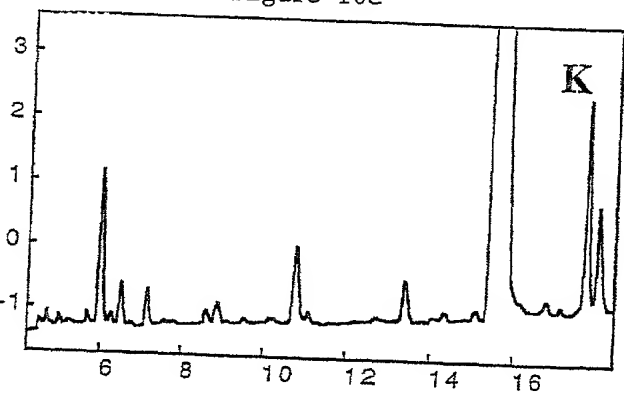


Figure 10f

14

18

0050.1618-001

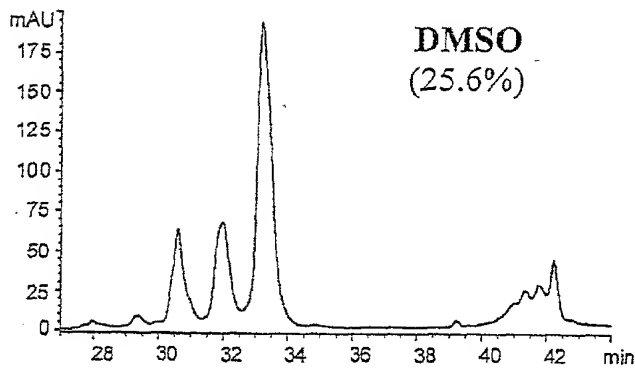


Figure 11a

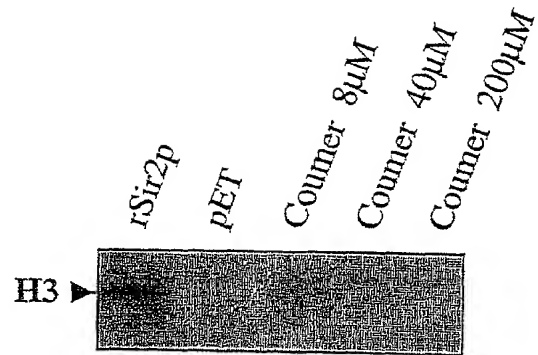


Figure 11c

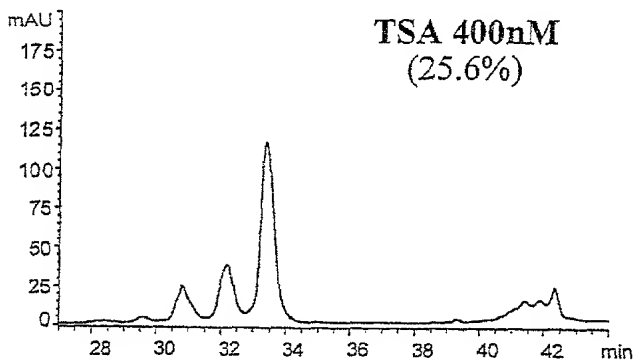


Figure 11b

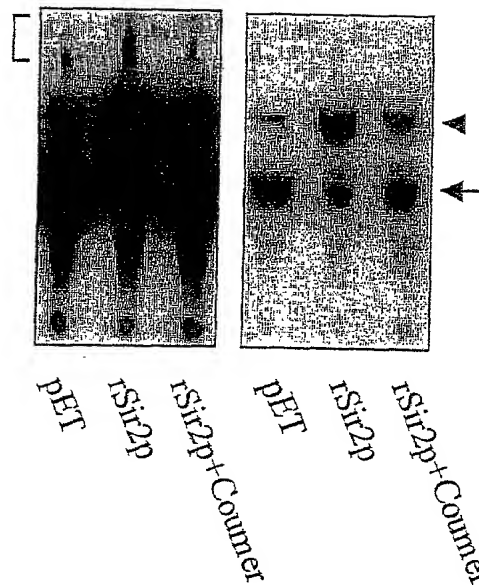


Figure 11d

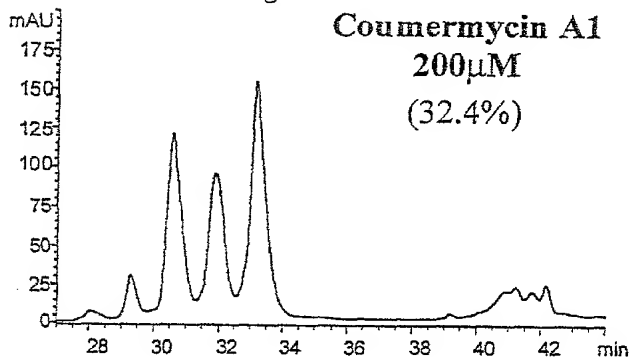


Figure 11e

0050.1618-001

1	M A D E V A L A L Q A A G S P A A A A M E A S Q P A D E P L R K P P R R D G
41	P G L G R S P G E P S A A V A P A A G C E A A S A A P A A L W R E A L G A A
81	A S A E R E A P A T A V A G D G N G S G L R R E P R A A D F D D D E G E E E
121	D E A A A A A A A A I G Y R D N L L I D G L L I N G F H S C E S D D D R T
161	S H A S S S D W T P R P R I G P Y T F V Q Q H L M I G T D P R T I L K D L L P E
201	T I P P E L D D M T L W Q I V I N I L S E P P K R K R K D I N T I E D A Y K
241	L L Q E C K K I V L T G A G V S V S C Q I P D F R S R D G I Y A R L A V D F P
281	D L P D Q A M F D I E Y F R K D P R P F F K F A K E I Y P G Q F O P S L C H K
321	F I A L S D K E G K L L R N Y T O N I D T L E Q V A G I Q R I L Q C H G S F A T
361	A S C L I C K Y K V D G E A V R G D I F N Q V Y P R C P R C A D E P L A I M K
401	P E I V F F G E N L P E O F H R A M K Y D K D E V D L L I V G S S L K V R P Y
441	A L I P S S I P H E V P Q I L N R E P I L P H L H F D V E L L G D C D V I N E
481	L C H R L G G E Y A K L C C N P V K L S E I T E K P P R P Q K E L V H L S E L P
521	P T P L H I S E D S S P E R T V P Q D S S V I A T L V D Q A T N N V N D L E
561	V S E S S C V E E K P Q E V T S R N V E N I N V E N P D F K A V G S S T A D K
601	N E R T S V A E T V R K C W P N R L A K E Q I S K R L E G N Q Y L F V P P N R Y
641	I F H G A E V Y S D S E D V L S S S C G S N S D S G T C Q S P S L E E P L E
681	D E S E I E E F Y N G L E D D T E R P E C A G G S G F G A D G D Q E V V N E A
721	I A T R Q E L T D V N Y P S D K S

Figure 12a

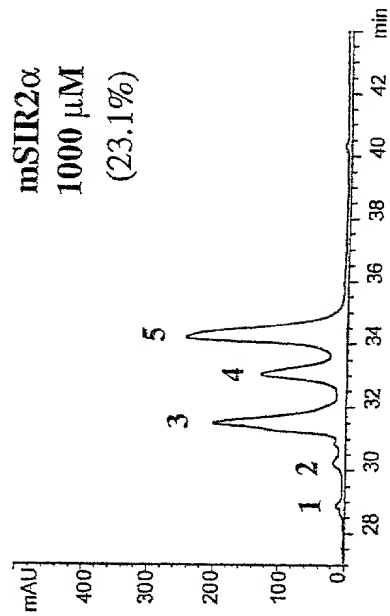


Figure 12c

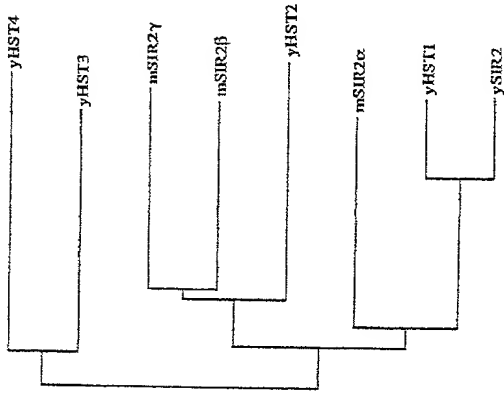


Figure 12b

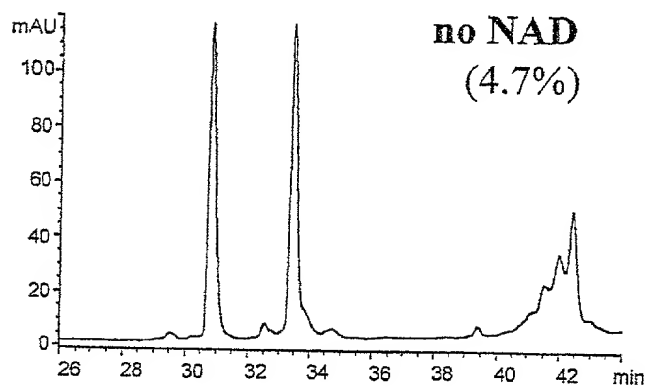


Figure 13a

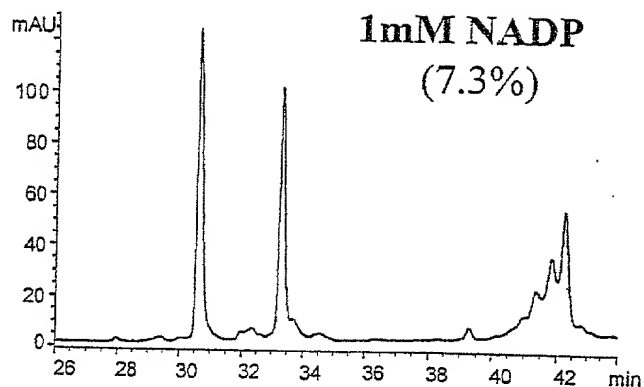


Figure 13d

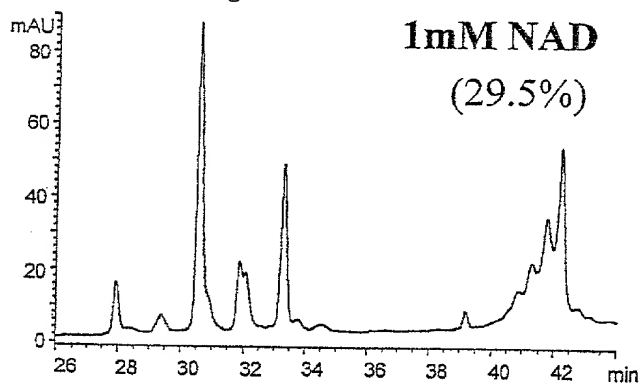


Figure 13b

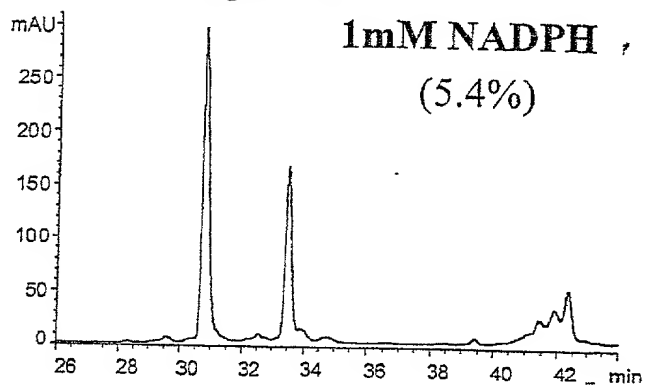


Figure 13e

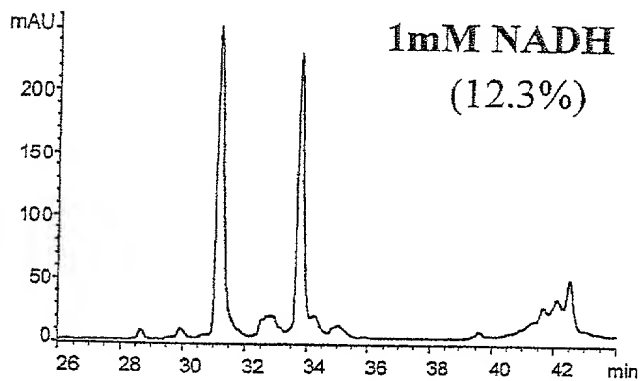
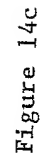
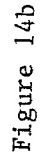
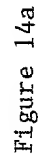


Figure 13c



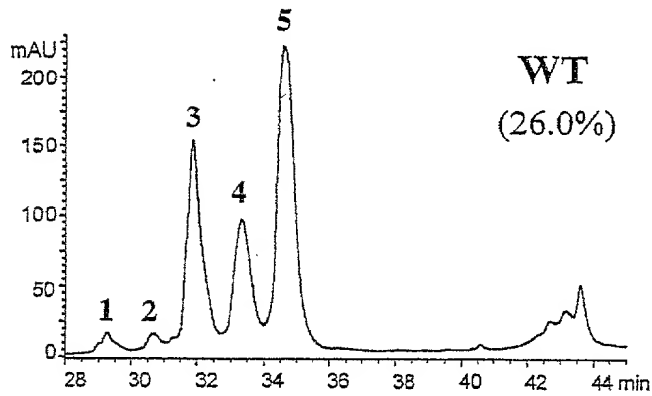


Figure 15a

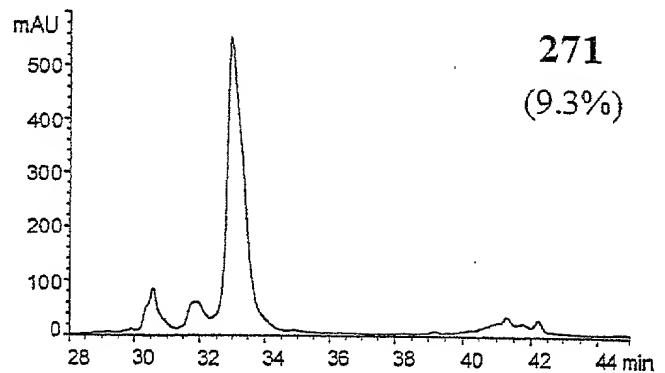


Figure 15e

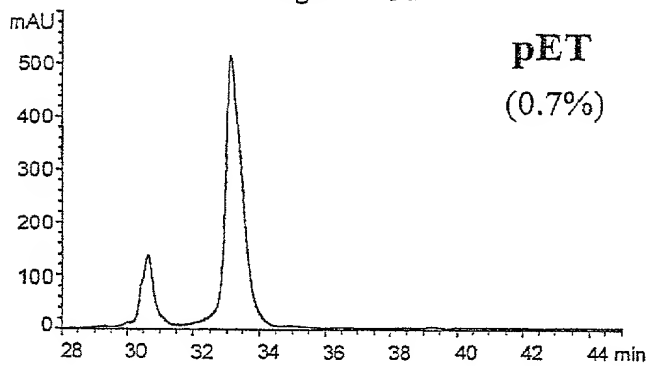


Figure 15b

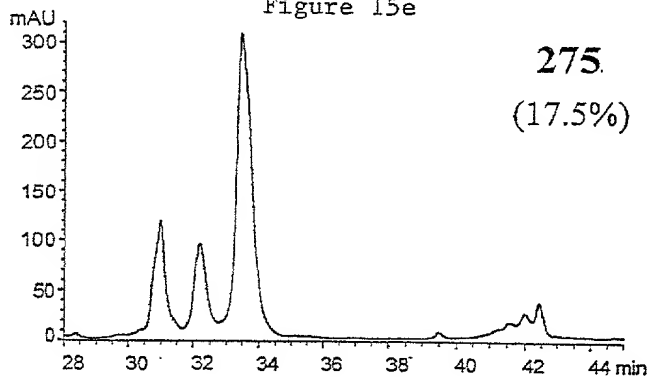


Figure 15f

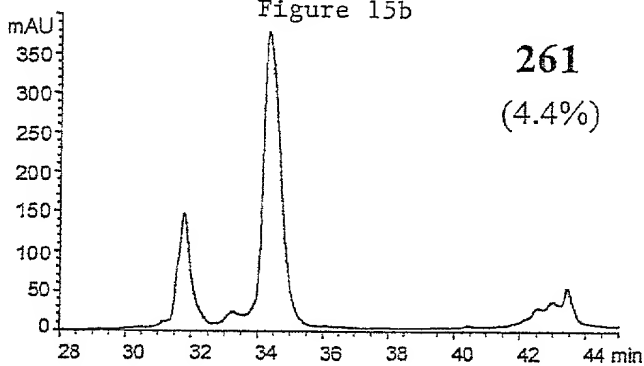


Figure 15c

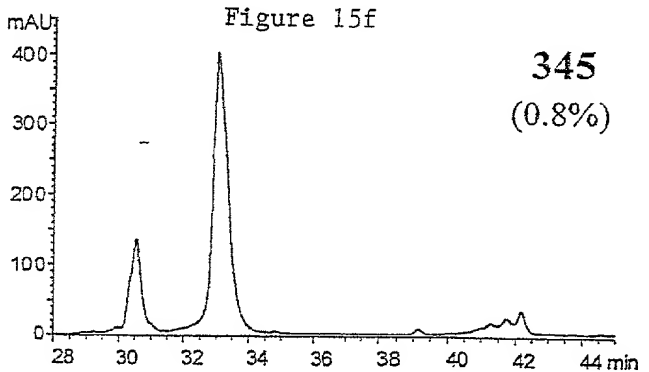


Figure 15g

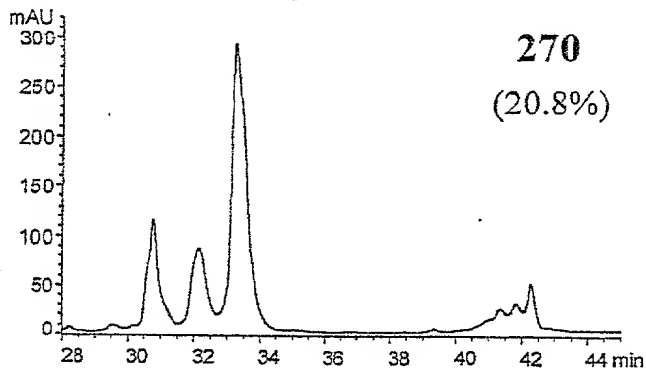


Figure 15d

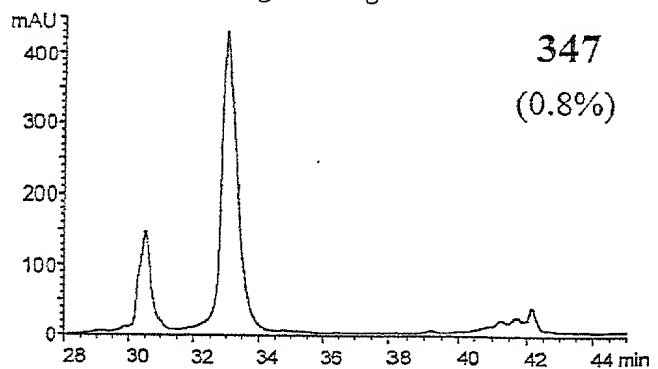


Figure 15h

00735786-1300

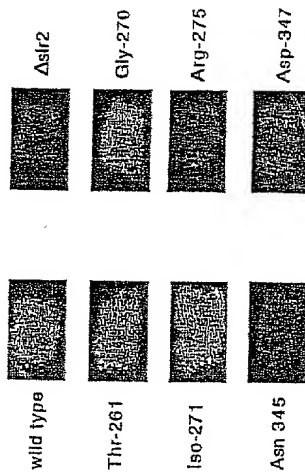


Figure 16b

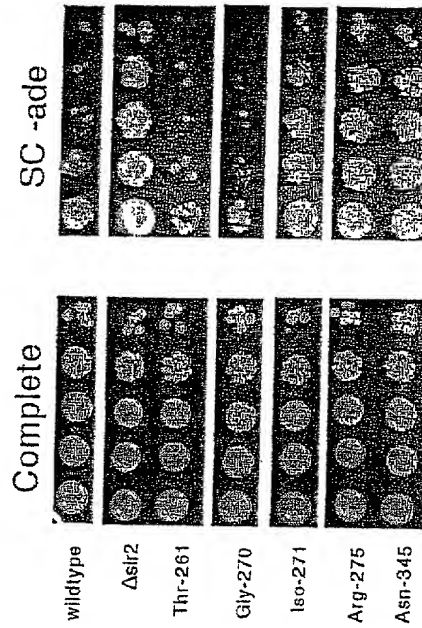


Figure 16d

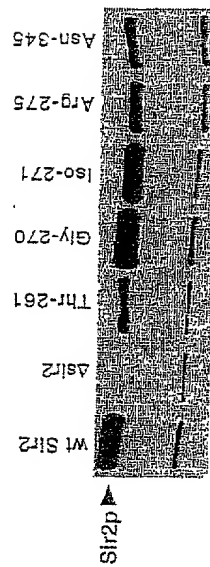


Figure 16a

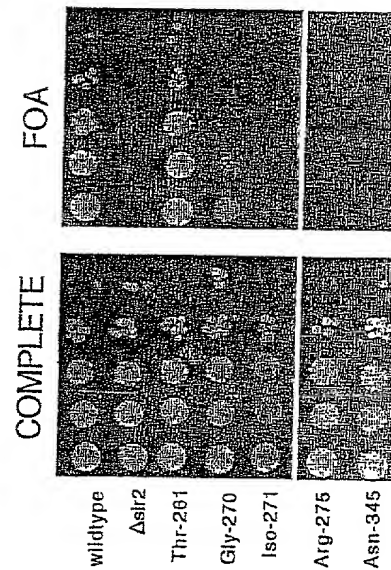


Figure 16c

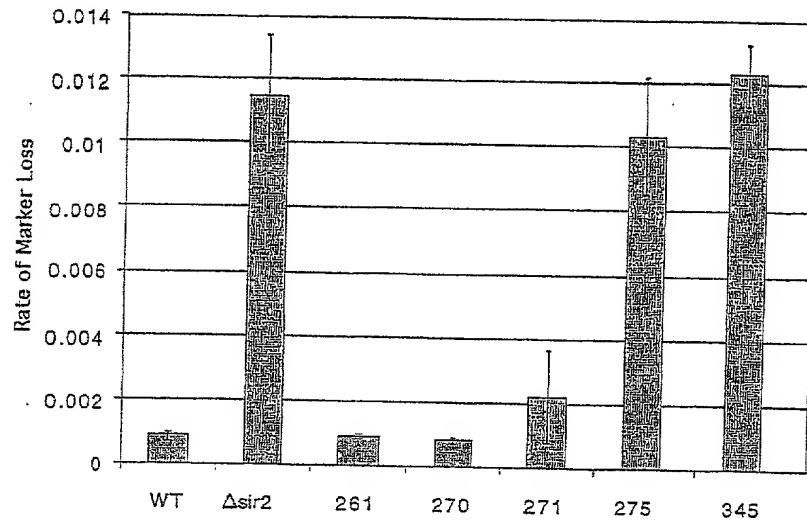


Figure 17a

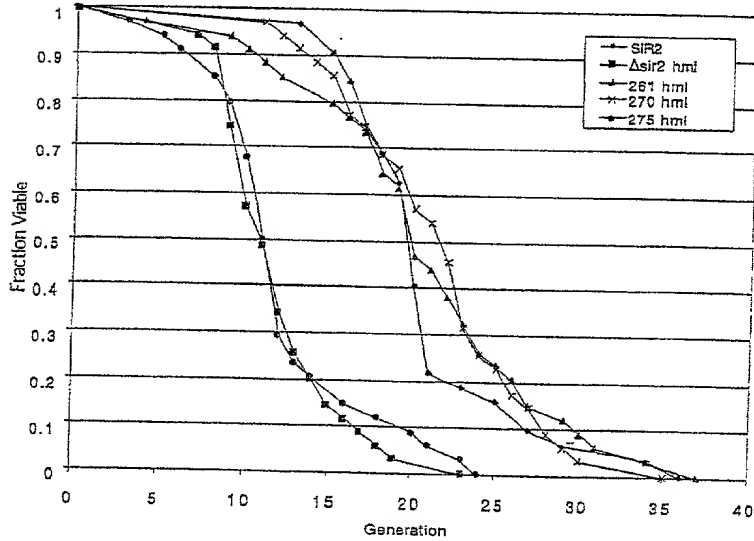


Figure 17b

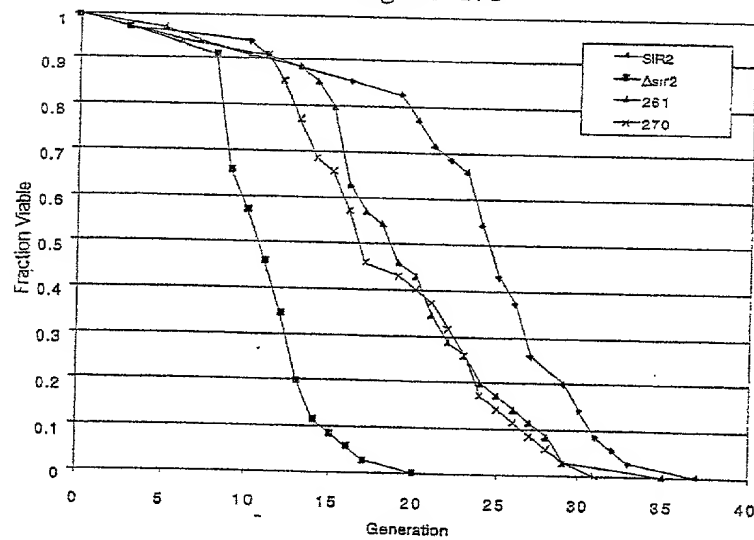


Figure 17c

0050.1618-001

0050.1618-001

Mutant	ADP-Rib. Activity (% of wt)	Deacetylase Activity (% of wt)	HM Silencing	Telomere Silencing	rDNA Silencing	rDNA Recombi- nation	Mean Life Span (HML+)
sir2Δ	0%	2.7%	-	-	-	1.15%	11.4
wildtype	100%	100%	+	+	+	0.09%	24.4
Thr-261	4%	17%	+	+	+	0.09%	19.8
Gly-270	7%	80%	+	+/-	+	0.08%	18.9
Iso-271	8%	36%	+	-	+/-	0.22%	ND
Arg-275	100%	67%	-	-	-	1.03%	ND
Asn-345	0%	3%	-	-	-	1.22%	ND
Asp-347	0%	3%	-	ND	ND	ND	ND

Figure 18

ySIR2	257	LEVLTGAGVSTSLGIPDFRS	SEGFYSKIKH	286
yHST1	203	LEVLTGAGVSTSLGIPDFRS	SEGFYSKIRH	232
yHST2	27	VIFMVGAGISTSCGIPDFRS	PCTGLYHNLAR	57
yHST3	55	LAOLTCAGISGNAGIPDFRS	SDGLYDLVKKDC	86
yHST4	95	MVVVSGAGISVAAGIPDFRS	SEGTFTYNGGS	126
mSIR2alpha	263	LEVLTGAGVSVSCGIPDFRS	RDGYARLAVDF	294
mSIR2beta	79	VICLVGAGISTSAGIPDFRS	PSTGLYANLEK	109
mSIR2g...	1		GTRLYSNLQQ	10
AI465098	48	VVFHTGAGISTASGIPDFRG	PHGVWTMEER	77
AI465820	67	LLVMTGAGISTESCIPDYRS	EKVGLYARTDR	97
AI466061	59	IAAISGAGVSAESGVPTFRG	AGGYWRKWQA	88
ySIR2	287	LGLDDPDQVFNYNIFMHDPSV	FYNTANM	314
yHST1	233	LGLDDPDQVFNLDIFLQDPSV	FYNIAHM	260
yHST2	58	LKLPYPEAVFDVDFEQSDPLP	FYT LAKE	85
yHST3	87	SQYWSIKSGREVEDSILRRDDFK	SIFAKEMER	119
yHST4	127	GKDLFDYNRYGDESISLKFN	QLMVSLE	154
mSIR2alpha	295	PDLPDPQAMVD EYFRKDP RP	FFKFAKE	322
mSIR2beta	110	HLPYPEAEFE SYFKKHPEP	FFALAKE	137
mSIR2g...	11	YDLPYPEAEFELGFFHNPKP	FFMLAKE	38
AI465098	78	GLAPKFDTEENA		90
AI465820	98	RPIQ-HIDFVPVLRASG		114
AI466061	89	QDLATPOAFA RNPSQWWEFYH	YRRE	113
ySIR2	315	VLP-PEKLYSPLHSFKMLQMKCKL	LBNYTON	345
yHST1	261	VLP-PENMYSPLHSFKMLQDKCKL	LBNYTON	291
yHST2	86	LYP-GNFRPSKKEHYLLKLFQDKDV	LKPVYTON	116
yHST3	120	LYSNVQLAKPTKTHKF AHLKDRNK	LRLCYTON	152
yHST4	155	RLS-KNCQPTKTFHEMLNEFARDGR	LRLLYTON	185
mSIR2alpha	323	LYP-GQFQPSLCHKFAALSDEKCKL	LRLNYTON	353
mSIR2beta	138	LYP-GQFKPTICHYFIRLEKEKGL	LRLCYTON	168
mSIR2g...	39	LYP-GHYRPNVTHYFLRLHDKEL	LRLLYTON	69
AI465098	91	-R-PSKTHMALVQLERMCFLSFL	VSON	115
AI465820	115	TWP-ENLWAGLNSPLTNPIQHTWL		137
AI466061	114	VMR-SK-EPNPGHLAAQCEAR		133
ySIR2	346	IDNLESYAGISTD	KLVO	362
yHST1	292	IDNLESYAGIDPD	KLVO	308
yHST2	117	DTLERQAGVKDD	LIE	133
yHST3	153	DGLEESIGLTL SNRKLP L TSFSSHWNLD	VVO	185
yHST4	186	DGLDTQLPHLS TN	VPLAKPIPS	211
mSIR2alpha	354	IDTLEQVAGIQR	KLQ	368
mSIR2beta	169	IDTLERVAGLEPQ	DLVE	185
mSIR2g...	70	IDGLERASGLPAS	KLVE	86
AI465098	116	VDGLDYRSGFPRD	KLAE	132
AI465820	0			137
AI466061	0			133

Figure 19

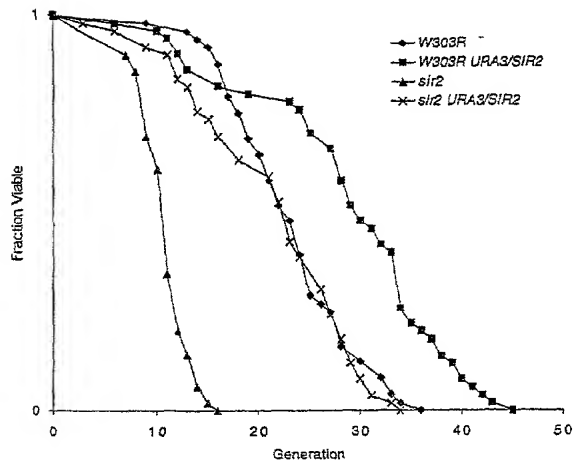


Figure 20

10 20 30 40 50 60
GCGGAGCAGAGGAGGCGAGGGCGGAGGGCCAGAGAGGCAGTTGGAAGATGGCGGACGAGG
M A D E V

70 80 90 100 110 120
TGGCGCTCGCCCTTCAGGCCGCGGCTCCCTTCCGCGGCGGCGCCATGGAGGCCGCGT
A L A L Q A A G S P S A A A A M E A A S

130 140 150 160 170 180
CGCAGCCGGCGGACGAGCCGCTCCGCAAGAGGCCCGCCGAGACGGGCCTGGCCTCGGGC
Q P A D E P L R K R P R R D G P G L G R

190 200 210 220 230 240
GCAGCCCGGGCGAGCCGAGCGCAGCAGTGGCGCCGCGCGCGCGGGTGTGAGGCGGCGA
S P G E P S A A V A P A A A G C E A A S

250 260 270 280 290 300
GCGCCGCGGCCCCGCGGCGCTGTGGCGGGAGGCGGCAGGGGCGGCGCGAGCGCGGAGC
A A A P A A L W R E A A G A A A S A E R

310 320 330 340 350 360
GGGAGGCCCCGCGACGGCCGTGGCCGGGGACGGAGACAATGGGTCCGCGCCTGCGGCGGG
E A P A T A V A G D G D N G S G L R R E

370 380 390 400 410 420
AGCCGAGGGCGGCTGACGACTTCGACGACGACGAGGGCGAGGAGGAGGACGAGGCGGCGG
P R A A D D F D D D E G E E E D E A A A

430 440 450 460 470 480
CGGCAGCGGCGGCGGCGAGCGATCGGCTACCGAGACAACCTCCTGTTGACCGATGGACTCC
A A A A A A I G Y R D N L L L T D G L L

490 500 510 520 530 540
TCACTAATGGCTTTTCATTCTGTGAAAGTGATGACGATGACAGAACGTCACACGCCAGCT
T N G F H S C E S D D D D R T S H A S S

550 560 570 580 590 600
CTAGTGAAGTGGACTCCGCGGCGCGGATAGGTCCATATACTTTTGTTCAGCAACATCTCA
S D W T P R P R I G P Y T F V Q Q H L M

610 620 630 640 650 660
TGATTGGCACCGATCCTCGAACAATTCTTAAAGATTTATTACCAGAAACAATTCTCTCCAC
I G T D P R T I L K D L L P E T I P P P

670 680 690 700 710 720
CTGAGCTGGATGATATGACGCTGTGGCAGATTGTTATTATATCCTTTTCAGAACCAACAA
E L D D M T L W Q I V I N I L S E P P K

730 740 750 760 770 780
AGCGGAAAAAGAAAAAGATATCAATACAATTGAAGATGCTGTGAAGTTACTGCAGGAGT
R K K R K D I N T I E D A V K L L Q E C

790 800 810 820 830 840
GTAAAAAGATAATAGTTCTGACTGGAGCTGGGGTTTCTGTCTCCTGTGGGATTCTGACT
K K I I V L T G A G V S V S C G I P D F

850 860 870 880 890 900
TCAGATCAAGAGACGGTATCTATGCTCGCCTTGCGGTGGACTTCCCAGACCTCCCAGACC
R S R D G I Y A R L A V D F P D L P D P

Figure 21a

910 920 930 940 950 960
 CTC AAGCCATGTTTGATATTGAGTATTTT AGAAAAGACCCAAGACCATTTCTTCAAGTTTG
 Q A M F D I E Y F R K D P R P F F K F A

970 980 990 1000 1010 1020
 CAAAGGAAATATATCCCGGACAGTTCAGCCGCTCTCTGTGTACAAAATTCATAGCTTTGT
 K E I Y P G Q F Q P S L C H K F I A L S

1030 1040 1050 1060 1070 1080
 CAGATAAGGAAGGAAAAC TACTTCGAAATTATACTCAAAATATAGATACCTTGGAGCAGG
 D K E G K L L R N Y T Q N I D T L E Q V

1090 1100 1110 1120 1130 1140
 TTGCAGGAATCCAAAGCATCCTTCAGTGT CATGGTTCCCTTTGCAACAGCATCTTGCCTGA
 A G I Q R I L Q C H G S F A T A S C L I

1150 1160 1170 1180 1190 1200
 TTTGTAAATACAAAGTTGATTGTGAAGCTGTTCTGTGGAGACATTTTTTAATCAGGTAGTTC
 C K Y K V D C E A V R G D I F N Q V V P

1210 1220 1230 1240 1250 1260
 CTCGGTGCCCTAGGTGCCCAGCTGATGAGCCACTTGCCATCATGAAGCCAGAGATTGTCT
 R C P R C P A D E P L A I M K P E I V F

1270 1280 1290 1300 1310 1320
 TCTTTGGTGAAAAC TTAACCAGAACAGTTTCATAGAGCCATGAAGTATGACAAAGATGAAG
 F G E N L P E Q F H R A M K Y D K D E V

1330 1340 1350 1360 1370 1380
 TTGACCTCCTCATTTGTTATTGGATCTTCTCTGAAAGTGAGACCAGTAGCACTAATTCCAA
 D L L I V I G S S L K V R P V A L I P S

1390 1400 1410 1420 1430 1440
 GTTCTATACCCCATGAAGTGCCTCAAATATTAAATAAATAGGGAACCTTTGCCTCATCTAC
 S I P H E V P Q I L I N R E P L P H L H

1450 1460 1470 1480 1490 1500
 ATTTTGTATGTAGAGCTCCTTTGGAGACTGCGATGTTATAATTAATGAGTTGTGT CATAGGC
 F D V E L L G D C D V I I N E L C H R L

1510 1520 1530 1540 1550 1560
 TAGGTGGTGAATATGCCAAACTTTGTTGTAACCTGTAAAGCTTTTCAGAAATTACTGAAA
 G G E Y A K L C C N P V K L S E I T E K

1570 1580 1590 1600 1610 1620
 AACCTCCACGCCCACAAAAGGAATTGGTTTCATTTATCAGAGTTGCCACCAACACCTCTTC
 P P R P Q K E L V H L S E L P P T P L H

1630 1640 1650 1660 1670 1680
 ATATTTTCGGAAGACTCAAGTTACCTGAAAGAACTGTACCACAAGACTCTTCTGTGATTG
 I S E D S S S P E R T V P Q D S S V I A

1690 1700 1710 1720 1730 1740
 CTACACTTGTAGACCAAGCAACAAACAATGTTAATGATTTAGAAGTATCTGAATCAA
 T L V D Q A T N N N V N D L E V S E S S

1750 1760 1770 1780 1790 1800
 GTTGTGTGGAAGAAAAACCACAAGAAGTACAGACTAGTAGGAATGTTGAGAACATTAAATG
 C V E E K P Q E V Q T S R N V E N I N V

1810 1820 1830 1840 1850 1860
 TGGAAAATCCAGATTTTAAAGGCTGTTGGTTCCAGTACTGCAGACAAAATGAAAGAACTT
 E N P D F K A V G S S T A D K N E R T S

1870 1880 1890 1900 1910 1920
 CAGTTGCAGAAACAGTGAGAAAATGCTGGCCTAATAGACTTGCAAAGGAGCAGATTAGTA
 V A E T V R K C W P N R L A K E Q I S K

Figure 21b

1930 1940 1950 1960 1970 1980
AGCGGCTTGAGGGTAATCAATACCTGTTTGTACCACCAAATCGTTACATATTCCACGGTG
R L E G N Q Y L F V P P N R Y I F H G A

1990 2000 2010 2020 2030 2040
CTGAGGTATACTCAGACTCTGAAGATGACGCTTGTCTCTAGTTCTCTGTGGCAGTAACA
E V Y S D S E D D V L S S S S C G S N S

2050 2060 2070 2080 2090 2100
GTGACAGTGGCACATGCCAGAGTCCAAGTTTAGAAGAACCCTTGAAGATGAAAGTGAAA
D S G T C Q S P S L E E P L E D E S E I

2110 2120 2130 2140 2150 2160
TTGAAGAATTCTACAATGGCTTGAAGATGATACGGAGAGGCCCGAATGTGCTGGAGGAT
E E F Y N G L E D D T E R P E C A G G S

2170 2180 2190 2200 2210 2220
CTGGATTGAGCTGATGGAGGGGATCAAGAGGTTGTTAATGAAGCTATAGCTACAAGAC
G F G A D G G D Q E V V N E A I A T R Q

2230 2240 2250 2260 2270 2280
AGGAATTGACAGATGTAACTATCCATCAGACAAATCATAACACTATTGAAGCTGTCCGG
E L T D V N Y P S D K S *

2290 2300 2310 2320 2330 2340
ATTGAGGAATTGCTCCACCAGCATTTGGGAACCTTTAGCATGTCAAAAAAATGAATGTTTAC

2350 2360 2370 2380 2390 2400
TTGTGAACCTGAACAAGGAAATCTGAAAGATGTATTATTTATAGACTGGAAAATAGATTG

2410 2420 2430 2440 2450 2460
TCTTCTTGGATAAATTTCTAAAGTTCCATCATTTCTGTTTGTACTTGTACATTCAACACTG

2470 2480 2490 2500 2510 2520
TTGGTTGACTTCATCTTCTTTCAAGGTTTCATTTGTATGATACATTCTGTATGTATGTATA

2530 2540 2550 2560 2570 2580
ATTTTGTTTTTTGCCTAATGAGITTC AACCTTTTAAAGTTTTCAAAGCCATTGGAATGT

2590 2600 2610 2620 2630 2640
TAATGTAAAGGGAACAGCTTATCTAGACCAAAGAATGGTATTTTCACACTTTTTTGTTTGT

2650 2660 2670 2680 2690 2700
AACATTGAATAGTTTAAAGCCCTCAATTTCTGTTCTGCTGAACTTTTATTTTATAGGACAG

2710 2720 2730 2740 2750 2760
TTAACTTTTTTAAACACTGGCATTTTCCAAAACCTGTGGCAGCTAACTTTTTTAAATCACA

2770 2780 2790 2800 2810 2820
GATGACTTGTAAATGTGAGGAGTCAGCACCGTGTCTGGAGCACTCAAACCTTGGGCTCAGT

2830 2840 2850 2860 2870 2880
GTGTGAAGCGTACTTACTGCATCGTTTTTGTACTTGTCTGCAGACGTGGTAATGTCCAAAC

2890 2900 2910 2920 2930 2940
AGGCCCCGTGAGACTAATCTGATAAATGATTTTGAAATGTGTTTCAAGTTGTTCTAGAAACA

2950 2960 2970 2980 2990 3000
ATAGTGCCCTGTCTATATAGGTCCCCCTTAGTTTGAATATTTGCCATTGTTTAAATTAATAAC

3010 3020 3030 3040 3050 3060
CTATCACTGTGGTAGAGCCCTGCATAGATCTTCACCACAAATACTGCCAAGATGTGAATAT

3070 3080 3090 3100 3110 3120
GCAAAGCCCTTTCTGAATCTAATAATGGTACTTCTACTGGGAGAGCTGTAATATTTTGGAC

3130 3140 3150 3160 3170 3180
TGCTGTTTTTCCATTAATGAGGAAAGCAATAGGCCTCTTAATTAAAGTCCCAAAGTCATA

Figure 21c

3190 3200 3210 3220 3230 3240
AGATAAATTGTAGCTCAACCAGAAAGTACACTGTTGCCTGTTGAGGATTTGGTGTAAATGT
3250 3260 3270 3280 3290 3300
ATCCCAAGGTGTTAGCCTTGTATTATGGAGATGAATACAGATCCAATAGTCAAATGAAAC
3310 3320 3330 3340 3350 3360
TAGTTCTTAGTTAATTTAAAAGCTTAGCTTGCCTTAAAAC TAGGGATCAATTTTCTCAACT
3370 3380 3390 3400 3410 3420
GCAGAAACTTTTAGCCTTTCAAACAGTTTACACCTCAGAAAGTCAGTATTTATTTTACAG
3430 3440 3450 3460 3470 3480
ACTTCTTTTGGAACATTGCCCCCAAATTTAAATATTTCATGTGGGTTTAGTATTTATTACAA
3490 3500 3510 3520 3530 3540
AAAAATGATTTGAAATATAGCTGTTCTTTATGCATAAAATACCCAGTTAGGACCATTACT
3550 3560 3570 3580 3590 3600
GCCAGAGGAGAAAAGTATTAAGTAGCTCATTTCCCTACCTAAAAGATAACTGAATTTATT
3610 3620 3630 3640 3650 3660
TGGCTACACTAAAGAATGCAGTATATTTAGTTTTCCATTTGCATGATGTGTTTGTGCTAT
3670 3680 3690 3700 3710 3720
AGACAATATTTTAAATTGAAAAATTTGTTTTAAATTATTTTACAGTGAAGACTGTTTTTC
3730 3740 3750 3760 3770 3780
AGCTCTTTTTTATATTGTACATAGACTTTTATGTAATCTGGCATATGTTTTGTAGACCGTT
3790 3800 3810 3820 3830 3840
TAATGACTGGATTATCTTCCTCCAACTTTTGAAATACAAAAACAGTGTGTTTTATACTAAAA
3850 3860 3870
AAAAAAAAGTCGACGCGCGCGCGAATTC

10 20 30 40 50 60
CCACGCGTCCGCGGACGCGTGGGCACGGGACAGAGCAGTCGGTGACAGTCCCGAGGGCCC
T R P R T R G H G T E Q S V T V P R A P

70 80 90 100 110 120
CCACCCCGTTCCCATGGCCGAGCCGACCGATTTCAGACTCGGACACTGAGGGAGGAGCCA
T P F P W P S R T D S D S D T E G G A T

130 140 150 160 170 180
CTGGTGAGAGGCAGAGATGGACTTCCTGAGGAATTTATTACCCAGACCCTGGGCCTGG
G G E A E M D F L R N L F T Q T L G L G

190 200 210 220 230 240
GTTCCCAAAGGAGCGTCTTCTAGACGAGCTGACCCTCGAAGGAGTGACACGCTACATGC
S Q K E R L L D E L T L E G V T R Y M Q

250 260 270 280 290 300
AGAGCGAGCGCTGCCGCAAGGTCATCTGTTTGGTGGGAGCCGGAATCTCCACGTCCGCGG
S E R C R K V I C L V G A G I S T S A G

310 320 330 340 350 360
GTATCCCTGACTTCCGCTCCCCGTCCACTGGCCTCTATGCAAACCTGGAGAAGTACCACC
I P D F R S P S T G L Y A N L E K Y H L

370 380 390 400 410 420
TTCCTTACCCAGAGGCCATCTTTGAGATCAGCTACTTCAAGAAACATCCGGAACCCCTTCT
P Y P E A I F E I S Y F K K H P E P F F

430 440 450 460 470 480
TTGCCCTTGCCAAGGAGCTCTATCCCGGGCAGTTCAAGCCAACCATCTGCCACTACTTCA
A L A K E L Y P G Q F K P T I C H Y F I

490 500 510 520 530 540
TCCGCCTGCTGAAGGAGAAGGGGCTGCTGCTGCGCTGCTACACGCAGAACATAGACACGC
R L L K E K G L L L R C Y T Q N I D T L

550 560 570 580 590 600
TGGAACGAGTGCGGGGCTGGAGCCCCAGGACCTGGTGGAGGCCACGGCACCTTCTACA
E R V A G L E P Q D L V E A H G T F Y T

610 620 630 640 650 660
CATCAGACTGTGTCAACACCTCCTGCAGAAAAGAATACACGATGGGCTGGATGAAAGAGA
S H C V N T S C R K E Y T M G W M K E K

670 680 690 700
AGATTTCTCAGAAGCAACTCCAGGTGTGAGCAGTGTCA
I S Q K Q L P G V S S V

Figure 22

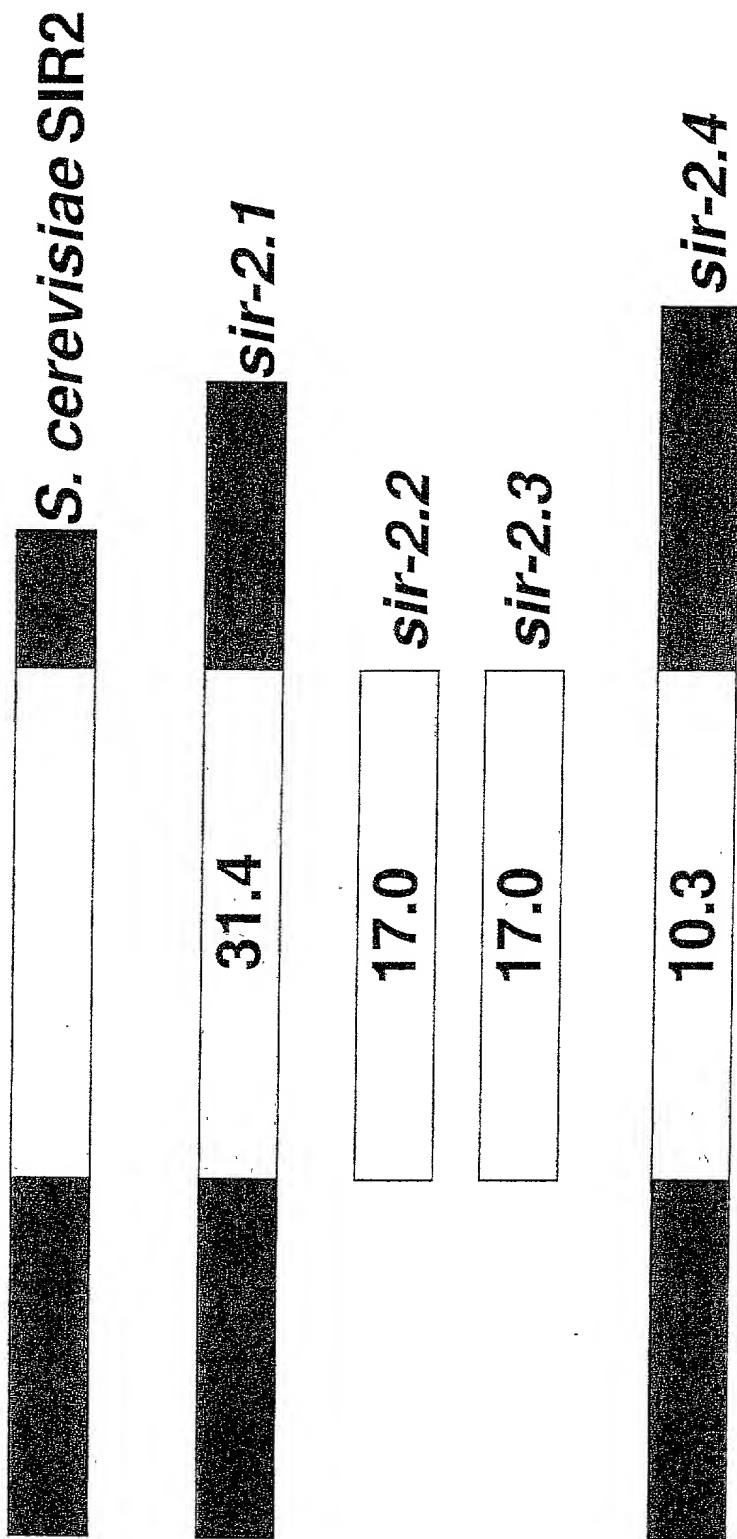


Figure 23

Figure 24A

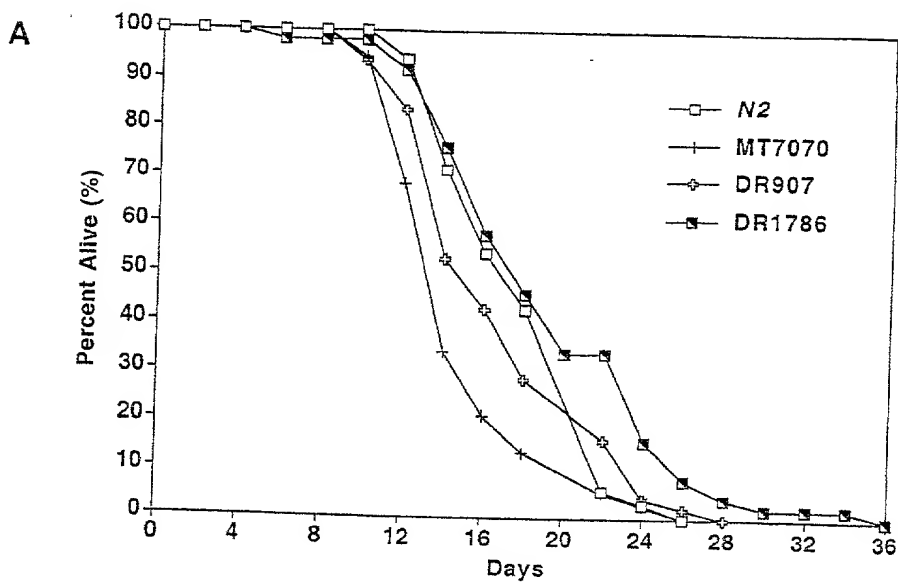


Figure 24B

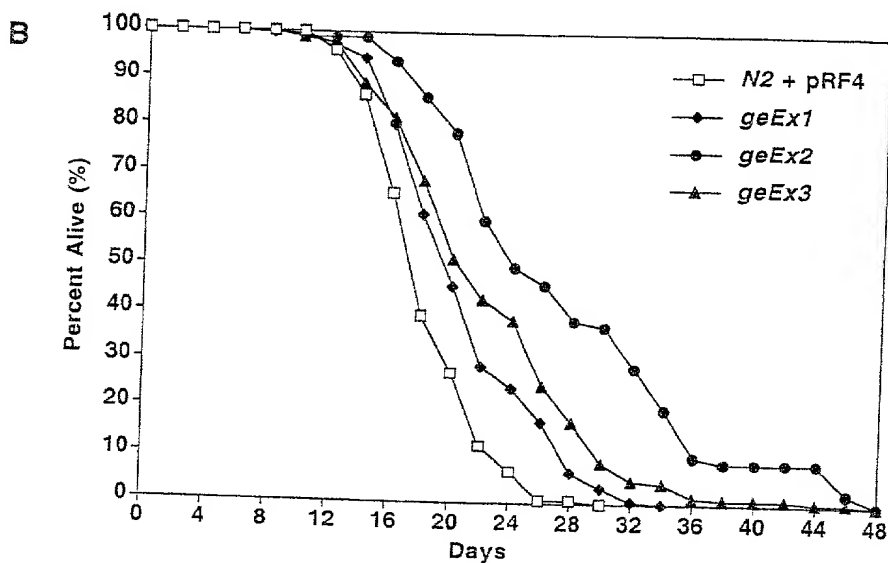


Figure 24C

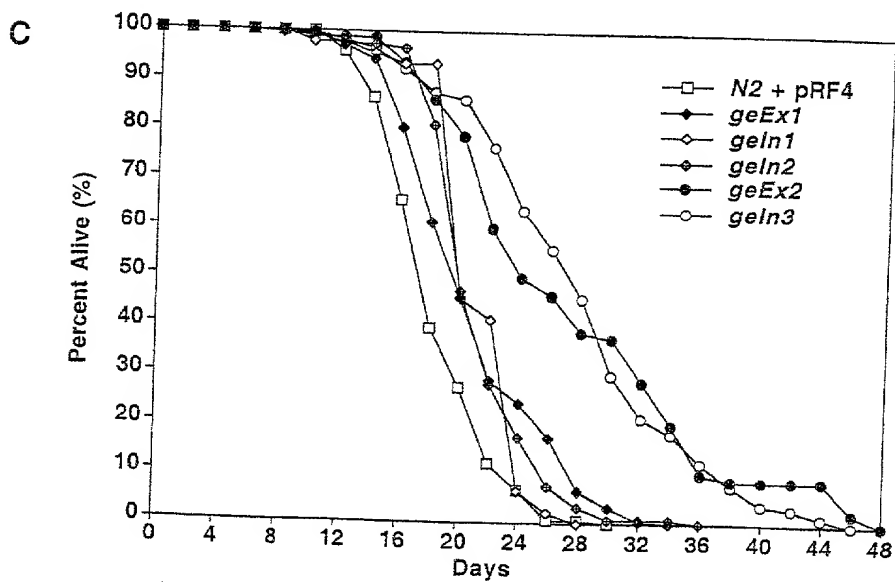


Figure 25A

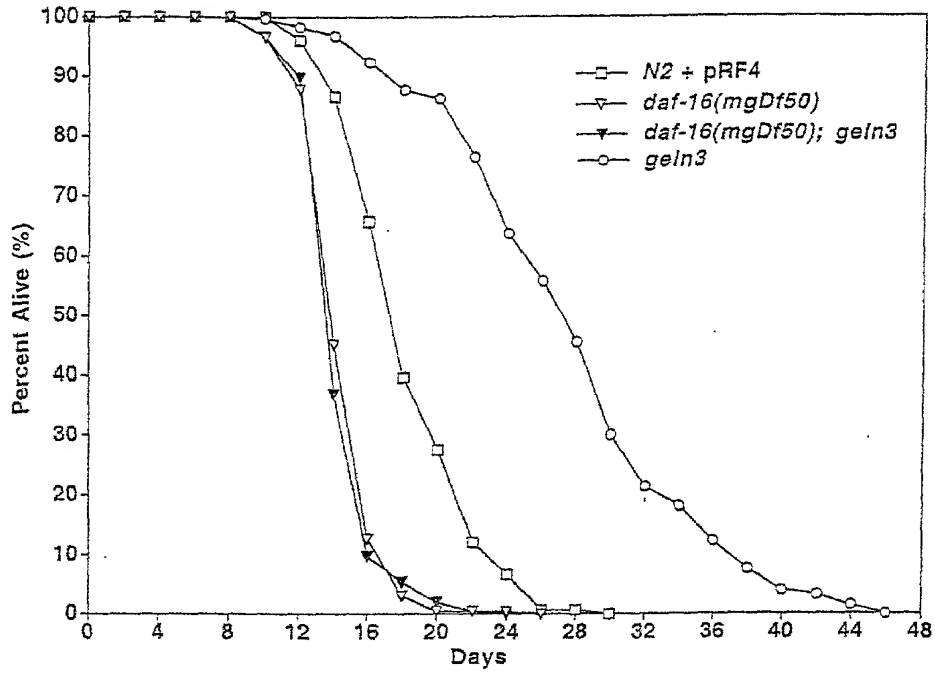


Figure 25B

